0360/0590

OIPE

ENTERED

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 3 <110> APPLICANT: Schall, Thomas J.
 4        Penfold, Mark E.T.
 5        ChemoCentryx, Inc.
 7 <120> TITLE OF INVENTION: Inhibition of CMV Infection and Dissemination
 9 <130> FILE REFERENCE: 019934-002510US
11 <140> CURRENT APPLICATION NUMBER: US 09/944,049
12 <141> CURRENT FILING DATE: 2001-08-30
14 <150> PRIOR APPLICATION NUMBER: US 60/229,365
15 <151> PRIOR FILING DATE: 2000-08-30
17 <160> NUMBER OF SEQ ID NOS: 48
19 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <213> ORGANISM: Human cytomegalovirus
26 <220> FEATURE:
27 <223> OTHER INFORMATION: human cytomegalovirus (HCMV) Toledo strain open
28        reading frame US28 (AU4.1)
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
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33 <223> OTHER INFORMATION: HCMV Toledo US28
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38 ggcgttgtct ttctgttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
39 cgacgtcgga ttcaatgctc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
40 cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
41 agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
42 tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atatcggcct 420
43 gtaaaacagg cctgcctttt cagtattttt tggtggatct ttgccgtgat catcgccatt 480
44 ccacatttta tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
45 gaggtcagct acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
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52 taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac atcttccgac 1020
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RAW SEQUENCE LISTING   DATE: 03/06/2002
PATENT APPLICATION: US/09/944,049   TIME: 13:04:54

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Output Set: N:\CRF3\03062002\I944049.raw

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72 Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
73          35                  40                  45
75 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
76      50                  55                  60
78 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
79 65                  70                  75                  80
81 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
82              85                  90                  95
84 Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
85              100                 105                 110
87 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
88          115                 120                 125
90 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
91      130                 135                 140
93 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
94 145                 150                 155                 160
96 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
97              165                 170                 175
99 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
100             180                 185                 190
102 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
103         195                 200                 205
105 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
106     210                 215                 220
108 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
109 225                 230                 235                 240
111 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
112             245                 250                 255
114 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
115         260                 265                 270
117 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
118         275                 280                 285
120 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
121     290                 295                 300
123 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
124 305                 310                 315                 320
126 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
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RAW SEQUENCE LISTING   DATE: 03/06/2002
PATENT APPLICATION: US/09/944,049   TIME: 13:04:54

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142       reading frame US28
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(1065)
147 <223> OTHER INFORMATION: HCMV VHL/E US28
149 <400> SEQUENCE: 3
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152 ggcgttgtct ttctcttcgg ttccatcggc aacttcttgg tgatcttcac catcacctgg 180
153 cgacgtcgga ttcaatgttc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
154 cttttcgttt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
155 agcgtgccgt gtacgttact cactgcctgt ttctacgtgg ctatgtttgc cagtttgtgt 360
156 tttatcacgg agattgcact cgatcgctac tacgctattg tttacatgag atatcggcct 420
157 gtaaaacagg cctgcctttt cagtattttt tggtggatct ttgccgtgat catcgccatt 480
158 ccacacttta tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
159 gaggtcagtt acccgatcat cctcaacgta gaactcatgc tcggtgcttt cgtgatcccg 600
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161 cgccacaaag ccgcattgt acgggtactt atagcggtcg tgcttgtctt tatcatcttt 720
162 tggctgccgt accacctgac gctgtttgtg gacacgttga aactgctcaa atggatctcc 780
163 agcagctgcg agttcgaaaa atcactcaag cgcgcgctca tcttgaccga gtcactcgcc 840
164 ttttgtcact gttgtctcaa tccgctgctg tacgtcttcg tgggcaccaa gtttcggcaa 900
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166 taccacagca tgagcttttc gcgtcggagc tcgccgagcc gaagagagac gtcttccgac 1020
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186 Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
187         35                  40                  45
189 Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
190     50                  55                  60
192 Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
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193  65                   70                   75                   80
195 Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
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199              100                  105                  110
201 Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
202          115                  120                  125
204 Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
205          130                  135                  140
207 Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
208 145                  150                  155                  160
210 Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
211              165                  170                  175
213 Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
214          180                  185                  190
216 Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
217          195                  200                  205
219 Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
220      210                  215                  220
222 Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
223 225                  230                  235                  240
225 Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
226              245                  250                  255
228 Lys Trp Ile Ser Ser Ser Cys Glu Phe Glu Lys Ser Leu Lys Arg Ala
229          260                  265                  270
231 Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
232          275                  280                  285
234 Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
235      290                  295                  300
237 Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
238 305                  310                  315                  320
240 Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
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252 <213> ORGANISM: Rhesus cytomegalovirus
254 <220> FEATURE:
255 <223> OTHER INFORMATION: rhesus monkey cytomegalovirus (rhCMV) US28 homolog
256         rhUS28.1
258 <220> FEATURE:
259 <221> NAME/KEY: CDS
260 <222> LOCATION: (1)..(1020)
261 <223> OTHER INFORMATION: rhUS28.1
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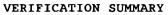Output Set: N:\CRF3\03062002\I944049.raw

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275 ctagttgtca tgacagtgtt cttttgggga ccgtttaata tcgtgttggt tattgacaat 720
276 attttacaga gatactatga taccacgaat tgcgatgtag aaaagattaa acatatcatg 780
277 gctatgatct cagaagccat tgtttatttt cgcggtatta cagcacctat tatttatgta 840
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300         35                  40                  45
302 Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
303      50                  55                  60
305 Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
306 65                  70                  75                  80
308 Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
309                  85                  90                  95
311 Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
312             100                 105                 110
314 Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
315          115                 120                 125
317 Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
318      130                 135                 140
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321 145                 150                 155                 160
323 Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
324                  165                 170                 175
326 Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
327             180                 185                 190
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/944,049

DATE: 03/06/2002
TIME: 13:04:55

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